

Package: ggseqlogo (via r-universe)

September 6, 2024

Type Package

Title A 'ggplot2' Extension for Drawing Publication-Ready Sequence Logos

Version 0.1

Date 2017-07-25

Author Omar Wagih

Maintainer Omar Wagih <omarwagih@gmail.com>

Description The extensive range of functions provided by this package makes it possible to draw highly versatile sequence logos. Features include, but not limited to, modifying colour schemes and fonts used to draw the logo, generating multiple logo plots, and aiding the visualisation with annotations. Sequence logos can easily be combined with other plots 'ggplot2' plots.

License LGPL

URL <https://github.com/omarwagih/ggseqlogo>

BugReports <https://github.com/omarwagih/ggseqlogo/issues>

Encoding latin1

Imports ggplot2

RoxygenNote 6.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

Repository <https://omarwagih.r-universe.dev>

RemoteUrl <https://github.com/omarwagih/ggseqlogo>

RemoteRef HEAD

RemoteSha 6658a39b6ea6e817b46150b85a913f6cad65e3f

Contents

geom_logo	2
ggseqlogo	3
list_col_schemes	4
list_fonts	4
make_col_scheme	5
pfms_dna	5
seqs_aa	6
seqs_dna	6
theme_logo	6
Index	7

geom_logo	<i>Plots sequence logo as a layer on ggplot</i>
-----------	---

Description

Plots sequence logo as a layer on ggplot

Usage

```
geom_logo(data = NULL, method = "bits", seq_type = "auto",
  namespace = NULL, font = "roboto_medium", stack_width = 0.95,
  rev_stack_order = F, col_scheme = "auto", low_col = "black",
  high_col = "yellow", na_col = "grey20", plot = T, ...)
```

Arguments

data	Character vector of sequences or named list of sequences. All sequences must have same width.
method	Height method, can be one of "bits" or "probability" (default: "bits")
seq_type	Sequence type, can be one of "auto", "aa", "dna", "rna" or "other" (default: "auto", sequence type is automatically guessed)
namespace	Character vector of single letters to be used for custom namespaces. Can be alphanumeric, including Greek characters.
font	Name of font. See list_fonts for available fonts.
stack_width	Width of letter stack between 0 and 1 (default: 0.95)
rev_stack_order	If TRUE, order of letter stack is reversed (default: FALSE)
col_scheme	Color scheme applied to the sequence logo. See list_col_schemes for available fonts. (default: "auto", color scheme is automatically picked based on seq_type). One can also pass custom color scheme objects created with the make_col_scheme function

low_col, high_col	Colors for low and high ends of the gradient if a quantitative color scheme is used (default: "black" and "yellow").
na_col	Color for letters missing in color scheme (default: "grey20")
plot	If FALSE, plotting data is returned
...	Additional arguments passed to layer params

Examples

```
# Load sample data
data(ggseqlogo_sample)

# Produce single sequence logo using geom_logo
p1 = ggseqlogo( seqs_dna[[1]] )
```

ggseqlogo

Quick sequence logo plot

Description

ggseqlogo is a shortcut for generating sequence logos. It adds the ggseqlogo theme [theme_logo](#) by default, and facets when multiple input data are provided. It serves as a convenient wrapper, so to customise logos beyond the defaults here, please use [geom_logo](#).

Usage

```
ggseqlogo(data, facet = "wrap", scales = "free_x", ncol = NULL,
  nrow = NULL, ...)
```

Arguments

data	Character vector of sequences or named list of sequences. All sequences must have same width
facet	Facet type, can be 'wrap' or 'grid'
scales	Facet scales, see facet_wrap
ncol	Number of columns, works only when facet='wrap', see facet_wrap
nrow	Number of rows, same as ncol
...	Additional arguments passed to geom_logo

Examples

```
# Load sample data
data(ggseqlogo_sample)

# Plot a single DNA sequence logo
p1 = ggseqlogo( seqs_dna[[1]] )
print(p1)

# Plot multiple sequence logos at once
p2 = ggseqlogo( seqs_dna )
print(p2)
```

list_col_schemes *List color schemes available in ggseqlogo*

Description

List color schemes available in ggseqlogo

Usage

```
list_col_schemes(v = T)
```

Arguments

v If true, font names are printed to stderr. Otherwise, color scheme names are returned as a character vector

list_fonts *List fonts available in ggseqlogo*

Description

List fonts available in ggseqlogo

Usage

```
list_fonts(v = T)
```

Arguments

v If true, font names are printed to stderr. Otherwise, font names are returned as a character vector

make_col_scheme	<i>Create new sequence logo color scheme</i>
-----------------	--

Description

Create new sequence logo color scheme

Usage

```
make_col_scheme(chars = NULL, groups = NULL, cols = NULL, values = NULL,
  name = "")
```

Arguments

chars	Vector of one letter characters
groups	Vector of groups for letters with same length as chars (optional if cols parameter is provided)
cols	Vector of colors with same length as chars (optional if values parameter is provided)
values	Vector of numerical values with same length as chars
name	Name of color scheme

Examples

```
# Discrete color scheme examples
cs1 = make_col_scheme(chars=c('A', 'T', 'G', 'C'), groups=c('g1', 'g1', 'g2', 'g2'),
  cols=c('red', 'red', 'blue', 'blue'), name='custom1')

cs2 = make_col_scheme(chars=c('A', 'T', 'G', 'C'), cols=c('red', 'red', 'blue', 'blue'),
  name='custom2')

# Quantitative color scheme
cs3 = make_col_scheme(chars=c('A', 'T', 'G', 'C'), values=1:4, name='custom3')
```

pfms_dna	<i>List of position frequency matrices for transcription factors</i>
----------	--

Description

List of position frequency matrices for transcription factors

seqs_aa	<i>List of aligned kinase-substrate binding sequences</i>
---------	---

Description

List of aligned kinase-substrate binding sequences

seqs_dna	<i>List of aligned transcription factor binding sequences</i>
----------	---

Description

List of aligned transcription factor binding sequences

theme_logo	<i>ggseqlogo custom theme</i>
------------	-------------------------------

Description

ggseqlogo custom theme

Usage

```
theme_logo(base_size = 12, base_family = "")
```

Arguments

base_size	font base size
base_family	font base family

Index

* data

pfms_dna, [5](#)

seqs_aa, [6](#)

seqs_dna, [6](#)

facet_wrap, [3](#)

geom_logo, [2](#), [3](#)

ggseqlogo, [3](#)

list_col_schemes, [4](#)

list_fonts, [4](#)

make_col_scheme, [5](#)

pfms_dna, [5](#)

seqs_aa, [6](#)

seqs_dna, [6](#)

theme_logo, [3](#), [6](#)